



MAR 23 2000  
TECH CENTER 1600/2900

# SEQUENCE LISTING

<110> Wallis, Nicola G.  
Burnham, Martin K. R.

<120> MurC

<130> GM10025

<140> US 09/103,287

<141> 1998-06-23

<150> US 60/052,720

<151> 1997-07-03

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<212> DNA

<213> Staphylococcus aureus

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catgaagaaa	tagtacgtgc	acatcaattg	aaattagatg	ttgtaagtta	taatgatttt	300
ttaggacaga	ttattgatca	atatacttca	gtagctgtaa	ctggtgcaca	tggtaaaact	360
tctacaacag	gtttattatc	acatggtatg	aatggtgata	aaaagacttc	atttttaatt	420
ggtgatggca	caggatggg	attgcctgaa	agtgattatt	tcgcttttga	ggcatgtgaa	480
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gatcatcctg	attatttcaa	agatattaat	gatgtttttg	atgcattcca	agaaatggca	600
cataatgtta	aaaaaggtat	tattgcttgg	ggtgatgatg	aacatctacg	taaaattgaa	660
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gcacaccatc	caagagaaat	tagtgctaca	attgacacag	cacgaaagaa	atatccacat	1020
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gaatttgcag	aaagtttatg	taaagcagat	cgtgtattct	tatgtgaaat	ttttggctca	1140
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tcgttcatta	atgaagatct	tattaatgta	ttagaacaat	ttgataatgc	tgttgtttta	1260
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<212> PRT

<213> Staphylococcus aureus

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35 40 45  
Lys Ile Leu Pro Phe Gly Ala Asn Asn Ile Lys Glu Asp Met Val Val  
50 55 60  
Ile Gln Gly Asn Ala Phe Ala Ser Ser His Glu Ile Val Arg Ala  
65 70 75 80  
His Gln Leu Lys Leu Asp Val Val Ser Tyr Asn Asp Phe Leu Gly Gln  
85 90 95  
Ile Ile Asp Gln Tyr Thr Ser Val Ala Val Thr Gly Ala His Gly Lys  
100 105 110  
Thr Ser Thr Thr Gly Leu Leu Ser His Val Met Asn Gly Asp Lys Lys  
115 120 125  
Thr Ser Phe Leu Ile Gly Asp Gly Thr Gly Met Gly Leu Pro Glu Ser  
130 135 140  
Asp Tyr Phe Ala Phe Glu Ala Cys Glu Tyr Arg Arg His Phe Leu Ser  
145 150 155 160  
Tyr Lys Pro Asp Tyr Ala Ile Met Thr Asn Ile Asp Phe Asp His Pro  
165 170 175  
Asp Tyr Phe Lys Asp Ile Asn Asp Val Phe Asp Ala Phe Gln Glu Met  
180 185 190  
Ala His Asn Val Lys Lys Gly Ile Ile Ala Trp Gly Asp Asp Glu His  
195 200 205  
Leu Arg Lys Ile Glu Ala Asp Val Pro Ile Tyr Tyr Tyr Gly Phe Lys  
210 215 220  
Asp Ser Asp Asp Ile Tyr Ala Gln Asn Ile Gln Ile Thr Asp Lys Gly  
225 230 235 240  
Thr Ala Phe Asp Val Tyr Val Asp Gly Glu Phe Tyr Asp His Phe Leu  
245 250 255  
Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala Val Ile  
260 265 270  
Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys Glu Ala  
275 280 285  
Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr Thr Ile  
290 295 300  
Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg Glu Ile  
305 310 315 320  
Ser Ala Thr Ile Asp Thr Ala Arg Lys Lys Tyr Pro His Lys Glu Val  
325 330 335  
Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala Phe Leu  
340 345 350  
Asn Glu Phe Ala Glu Ser Leu Cys Lys Ala Asp Arg Val Phe Leu Cys  
355 360 365  
Glu Ile Phe Gly Ser Ile Arg Glu Asn Ser Gly Ala Leu Thr Ile Gln  
370 375 380  
Asp Leu Ile Asp Lys Ile Gly Gly Ala Ser Phe Ile Asn Glu Asp Leu  
385 390 395 400  
Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Val Leu Phe Met Gly

B1

405                      410                      415  
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 ccatacagtt ttaaatgcat tagctgtaat tgcgattagt tatttagaga agctagatgt 180  
 tacaatatatt aaagaagcat tagaaacggt tgggtggtgt aaacgtcgtt tcaatgaaac 240  
 tacaattgca aatcaagtta ttgtagatga ttatgcacac catccaagag aaattagtgc 300  
 tacaattgac acagcacgaa agaaatatcc acataaagaa gttgttcgag tatttcaacc 360  
 acacactttc tctagaacac aagcattttt aaatgaattt gcagaaagt taagtaaagc 420  
 agatcgtgta ttcttatgtg aaatttttgg atcaattaga gaaaatactg gcgcattaac 480  
 gatacaagat ttaattgata aaattgaagg tgcatcggtt attaatagag attctattaa 540  
 tgtattagaa caatttgata atgctgttgt tttattttat ggtgcaggtg atattcaaaa 600  
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                          20                      25                      30  
 Phe Leu Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala  
                          35                      40                      45  
 Val Ile Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys  
                          50                      55                      60  
 Glu Ala Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr  
 65                      70                      75                      80  
 Thr Ile Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg  
                          85                      90                      95  
 Glu Ile Ser Ala Thr Ile Asp Thr Ala Arg Lys Lys Tyr Pro His Lys  
                          100                      105                      110  
 Glu Val Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala  
                          115                      120                      125  
 Phe Leu Asn Glu Phe Ala Glu Ser Leu Ser Lys Ala Asp Arg Val Phe  
                          130                      135                      140  
 Leu Cys Glu Ile Phe Gly Ser Ile Arg Glu Asn Thr Gly Ala Leu Thr  
 145                      150                      155                      160  
 Ile Gln Asp Leu Ile Asp Lys Ile Glu Gly Ala Ser Leu Ile Asn Glu  
                          165                      170                      175  
 Asp Ser Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Val Leu Phe  
                          180                      185                      190

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210 215

B1  
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